

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:52:14 ; Search time 170.72 seconds

(Without alignments)
17.898 Million cell updates/sec

Title: US-09-331-631a-1_COPY_29_73

Perfect score: 252

Sequence: 1 SEFDROEYECCKRQCQMOLET.....RCVSQCDKRFEDIDMSKYD 45

Scoring table: BLOSUM62

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77.5	30.8	509	2 S08059	alpha-globulin typ
2	77.5	30.8	588	1 FMCNAB	alpha-globulin B p
3	72	28.6	605	2 S06398	alpha-globulin typ
4	70.5	28.0	566	2 S22477	vicilin precursor
5	67.5	26.8	47	2 JCS557	arginine/glutamate
6	67	26.6	810	2 T44430	protein PV100 (imp
7	67	26.6	1170	1 TSHUP1	thrombospondin 1 p
8	67	26.6	1170	2 A40558	thrombospondin 1 p
9	64	25.4	554	2 T45840	grpase activating-
10	63	25.0	524	2 JQ1730	62K sucrose-bindin
11	59.5	23.6	3078	2 T28432	variant-specific s
12	58	23.0	242	2 T29699	hypotheical prote
13	58	23.0	1421	2 T05892	hypotheical prote
14	57	22.6	316	2 G71600	rifin PRB1005w - m
15	57	22.6	725	1 MWV294	A-type inclusion p
16	57	22.6	726	2 JQ2162	A-type inclusion p
17	57	22.6	1284	1 MWVZAI	A-type inclusion p
18	55	21.8	305	2 B55346	phosphoprotein pho
19	55	21.8	348	2 A71601	rifin PRB1015w - m
20	55	21.8	623	2 T06674	hypotheical prote
21	55	21.8	795	1 HHC408	heat shock protein
22	55	21.8	822	2 T02824	hypotheical prote
23	54.5	21.6	244	2 S44822	F44E2.3 protein -
24	54.5	21.6	1021	2 T15765	hypotheical prote
25	54.5	21.6	1259	2 T32901	hypotheical prote
26	54.5	21.6	2715	2 T13049	eyelid - fruit fly
27	54	21.4	291	2 S62730	cyclin DI - zebra
28	54	21.4	314	2 T02964	cyclin A-type (clo
29	54	21.4	643	2 T19225	Ro autoantigen 60K

30	54	21.4	880	2 F75103	probable purine NR
31	53.5	21.2	67	2 T15592	hypotheical prote
32	53.5	21.2	301	2 T54209	hypotheical prote
33	53.5	21.2	1642	2 T08880	NMDA receptor-bind
34	53	21.0	622	2 E69006	glutamate synthase
35	53	21.0	702	2 S46854	A29L protein - var
36	53	21.0	702	2 T82167	hypotheical prote
37	53	21.0	702	2 T28570	108K heat shock pr
38	53	21.0	795	2 T50255	ubiquinol--cytochr
39	52.5	20.8	91	1 S00219	colipase A precurs
40	52.5	20.8	96	1 XLH0A	probable prephenat
41	52.5	20.8	275	2 B81430	hypotheical prote
42	52.5	20.8	425	2 T18592	hypotheical prote
43	52.5	20.8	600	2 T18593	thrombospondin 2 p
44	52.5	20.8	1172	1 TSHUP2	antimicrobial pept
45	52	20.6	33	2 A41822	

ALIGNMENTS

RESULT 1
S08059
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N:Alternate names: seed storage protein
C:Species: Gossypium hirsutum (upland cotton)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: S08059
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.
A:Reference number: S06398
A:Accession: S08059
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-509 <CHL>
C:Superfamily: glycylcin

Query Match 30.8%; Score 77.5; DB 2; Length 509;
Best Local Similarity 41.2%; Pred. No. 0.11;
Matches 14; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

OY 5 ROEYECCKRQCQMOLETSGOMRCVSOCDKRFED 38
Db 3 QRRTECCQECRQOE-ERQOPCCQRCIKRFEQE 35

RESULT 2
FMCNAB
alpha-globulin B precursor (clone C72) - upland cotton
N:Alternate names: seed storage protein; vicilin precursor
C:Species: Gossypium hirsutum (upland cotton)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: A30838; S06911
R:Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII
A:Reference number: A30838
A:Accession: A30838
A:Molecule type: mRNA
A:Residues: 1-588 <CHL>
A:Cross-references: GB:M16891; NID:q167374; PIDN:AAA33071.1; PID:q167375
A:Experimental source: var. Coker 201
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.
A:Reference number: S06398
A:Accession: S06911
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-81 <CH2>
C:Comment: This is a seed storage protein.

A:Cross-references: GB:X04665; NID:q37137; PIDN:CAA28370.1; PID:q37138
 A:Note: parts of this sequence, including the amino end of the mature protein, were detected by R. Laherty, C.D.; Gileman, T.M.; Dixit, V.M.
 J. Biol. Chem. 264, 11222-11227, 1989
 A:Title: Characterization of the promoter region of the human thrombospondin gene. DNA S
 A:Reference number: A34274; MUID:89291870
 A:Accession: A34274
 A:Molecule type: DNA
 A:Residues: 1-166 <LAH>
 A:Cross-references: GB:J04835
 R:Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, J. Cell Biol. 108, 729-736, 1999
 A:Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in th
 A:Reference number: A30140; MUID:89139590
 A:Accession: A30140
 A:Molecule type: mRNA
 A:Residues: 1-83, 'A', 85-522, 'A', 524-1170 <HEN>
 A:Cross-references: EMBL:X14787; NID:q37464; PIDN:CAA32889.1; PID:q37465
 A:Note: parts of this sequence, including the amino end of the mature protein, were detected by R. Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
 Biochemistry 25, 8418-8425, 1986
 A:Title: Partial amino acid sequence of human thrombospondin as determined by analysis c
 A:Reference number: A25812; MUID:87157592
 A:Accession: A25812
 A:Molecule type: mRNA
 A:Residues: 1-83, 'A', 85-397 <ROB>
 A:Cross-references: GB:M25631; NID:q538353; PIDN:AAA63741.1; PID:q538354
 R:Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
 A:Reference number: A05172; MUID:86287276
 A:Accession: A05172
 A:Molecule type: mRNA
 A:Residues: 1-83, 'A', 85-374, 'RC', <DIX>
 A:Cross-references: GB:M14326; NID:q340005; PIDN:AAA61237.1; PID:q553801
 R:Sun, X.; Skorstengaard, K.; Mosher, D.F.
 J. Cell Biol. 118, 693-701, 1992
 A:Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
 A:Reference number: A42927; MUID:92348511
 A:Accession: A42927
 A:Molecule type: protein
 A:Residues: 967-1003 <SON>
 A:Note: Cys-992 is shown to have a free sulfhydryl
 C:Genetics:
 A:Gene: GDB:THBS1; TSP1; TSP
 A:Cross-references: GDB:120438; OMIM:188060
 A:Map position: 15q15-15q15
 A:Introns: 23/1
 A:Note: the list of introns may be incomplete
 C:Complex: homotrimer, disulfide linked
 C:Function:
 A:Description: participates in cell migration and adhesion, and in platelet aggregation
 C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; VC
 C:Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
 F:317-375/Domain: von Willebrand factor type C repeat homology <VWC>
 F:378-429/Domain: thrombospondin type 1 repeat homology <THR1>
 F:434-490/Domain: thrombospondin type 1 repeat homology <THR2>
 F:491-547/Domain: thrombospondin type 1 repeat homology <THR3>
 F:551-586/Domain: EGF homology <EGF1>
 F:650-689/Domain: EGF homology <EGF>
 F:926-928/Region: cell attachment (R-G-D) motif
 F:171-232/Disulfide bonds: #status predicted
 F:248-360,708,1067/Binding site: carbohydrate (Asn) #status predicted
 F:270,274/Disulfide bonds: interchain #status predicted
 F:510/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 F:1051/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 26.6%; Score 67; DB 1; Length 1170;
 Best Local Similarity 39.5%; Pred. No. 3.9;
 Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

QY 13 RQCMQLE----TSGQMRRC-VSQCDKRFEDIDWSKY 44
 | | | | | : | | | | | : | | | | | : | | | | | :
 DB 404 RSCDSLNRRCGSSVQTRTCHIDECDFKQDGGSMSHR 441

RESULT 8
 A40558
 thrombospondin 1 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 20-Aug-1999
 C:Accession: A40558; A37905; B42387; S68787
 R:Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
 Genomics 11, 587-600, 1991
 A:Title: Characterization of the murine thrombospondin gene.
 A:Reference number: A40558; MUID:92128941
 A:Accession: A40558
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1170 <LAM>
 A:Cross-references: GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453; GB:M62454;
 M62455; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:q511867; PIDN:AAA5
 R:Bornstein, P.; Alf, D.; Deva-raja, S.; Framson, P.; Li, P.
 J. Biol. Chem. 265, 16931-16939, 1990
 A:Title: Characterization of the mouse thrombospondin gene and evaluation of the role
 A:Reference number: A37905; MUID:90375546
 A:Accession: A37905
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-490 <BOR>
 A:Cross-references: GB:J05605; GB:J05606; NID:q201991; PIDN:AAA40431.1; PID:q554390
 R:Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
 J. Biol. Chem. 267, 3274-3281, 1992
 A:Title: Characterization of mouse thrombospondin 2 sequence and expression during ce
 A:Reference number: A42587; MUID:92147683
 A:Accession: B42587
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-1152, 'P', 1154-1170 <LAH>
 A:Cross-references: GB:M87276
 A:Note: sequence extracted from NCBI backbone (NCBI:P:81501)
 R:Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
 FEBS Lett. 387, 36-41, 1996
 A:Title: Expression and initial characterization of recombinant mouse thrombospondin
 A:Reference number: S68787; MUID:96234006
 A:Accession: S68787
 A:Molecule type: protein
 A:Residues: 19-26, 'X', 28-37 <CHE>
 C:Complex: homotrimer, disulfide linked
 C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology;
 C:Keywords: calcium binding; glycoprotein; homotrimer
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
 F:317-375/Domain: von Willebrand factor type C repeat homology <VWC>
 F:378-429/Domain: thrombospondin type 1 repeat homology <THR1>
 F:434-490/Domain: thrombospondin type 1 repeat homology <THR2>
 F:491-547/Domain: thrombospondin type 1 repeat homology <THR3>
 F:551-586/Domain: EGF homology <EGF>
 F:248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.6%; Score 67; DB 2; Length 1170;
 Best Local Similarity 39.5%; Pred. No. 3.9;
 Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

QY 13 RQCMQLE----TSGQMRRC-VSQCDKRFEDIDWSKY 44
 | | | | | : | | | | | : | | | | | : | | | | | :
 DB 404 RSCDSLNRRCGSSVQTRTCHIDECDFKQDGGSMSHR 441

RESULT 9
 T45840
 GTPase activating-like protein - Arabidopsis thaliana

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N:Alternate names: protein F2K15.210
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T45840
R|Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, W.; Zipp, M.; Newes, H.W.; Lemcke,
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23015
A:Accession: T45840
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-554 <EMB>
A:CROSS-references: EMBL:ALJ32956
C:Experimental source: cultivar Columbia; BAC clone F2K15
C:Genetics:
A:Map position: 3
A:Introns: 53/2; 98/3; 115/2; 133/2
A>Note: F2K15.210

Query Match          25.4%; Score 64; DB 2; Length 554;
Best Local Similarity 28.2%; Pred. No. 4.5;
Matches 11; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY      5 ROEYECKROGCMOLETSGOMRCVSCDCRFEEEDIMSK 43
       1:| | :| | :| |   :| |   :| | :| |
Db     148 RKEVERLRQCCKRLQKHNNGTFRKLNGSETTDIEDWDR 186

RESULT 10
JOI730
        62k sucrose-binding protein precursor - soybean
C:Species: Glycine max (soybean)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C:Accession: JOI730
R|Grimes, H.D.; Overvoorde, P.J.; Ripp, K.; Franceschi, V.R.; Hiltz, W.D.
Plant Cell 4, 1561-1574, 1992
A>Title: A 62-kD sucrose binding protein is expressed and localized in tissues actively
A:Reference number: JOI730; MUID:93104680
A:Accession: JOI730
A:Molecule type: mRNA
A:Residues: 1-524 <GR>
A:CROSS-references: GR:I06038; NID:g1431744; PIDN:AAB03894.1; PID:g170064
C:Superfamily: glycinin
C:Keywords: sugar transport
F1-29/Domain: signal sequence #status predicted <SIG>
F1-30-524/Product: 62k sucrose-binding protein #status predicted <MAT>

Query Match          25.0%; Score 63; DB 2; Length 524;
Best Local Similarity 38.2%; Pred. No. 5.6;
Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1;

QY      2 EFDRQEYECRKROCQMOLP--TSQGMRCVCVSODCK 33
       1:| | :| | :| |   :| |   :| | :| |
Bb     34 EEDEPELVTCRHCCQQQQQTTEGGDKRVCLQSDDR 67

RESULT 11
T28432
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)
N:Alternate names: erythrocyte membrane binding protein I (EMP1)
C:Species: Plasmodium falciparum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T28432
R|Su, X.Z.; Heistowle, V.M.; Wertheimer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson, D.S.
Cell 82, 89-100, 1995
A>Title: The large diverse gene family var encodes proteins involved in cytoadherence an
A:Reference number: Z20487; MUID:95330813
A:Accession: T28432
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-3078 <SNX>
A:CROSS-references: EMBL:L40608; NID:g886374; PID:g886375; PIDN:AAA75396.1

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[illegible]

